



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 06:13 AM UTC

PDB ID : 7VJE / pdb_00007vje
Title : class II photolyase MmCPDII semiquinone to fully reduced TR-SFX studies (300 ns time-point)
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Deposited on : 2021-09-28
Resolution : 2.50 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	: 4-5-2 with Phenix2.0
Mogul	: 2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	: 2.0
EDS	: 3.0
Buster-report	: wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	: 20250101.v01 (using entries in the PDB archive January 1st 2025)

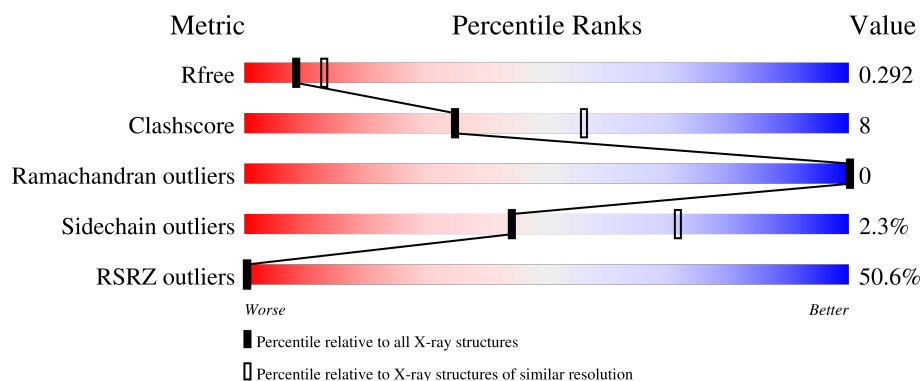
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	482	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	DTT	A	505	-	-	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 3836 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

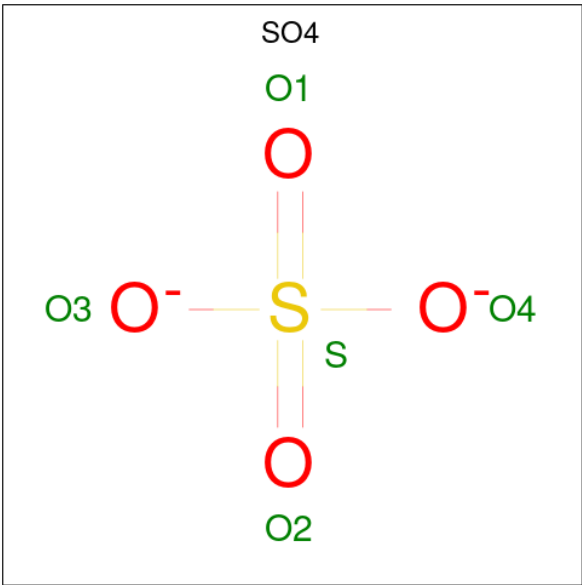
- Molecule 1 is a protein called DNA photolyase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	453	Total	C	N	O	S	0	7	0
			3572	2315	584	657	16			

There are 21 discrepancies between the modelled and reference sequences:

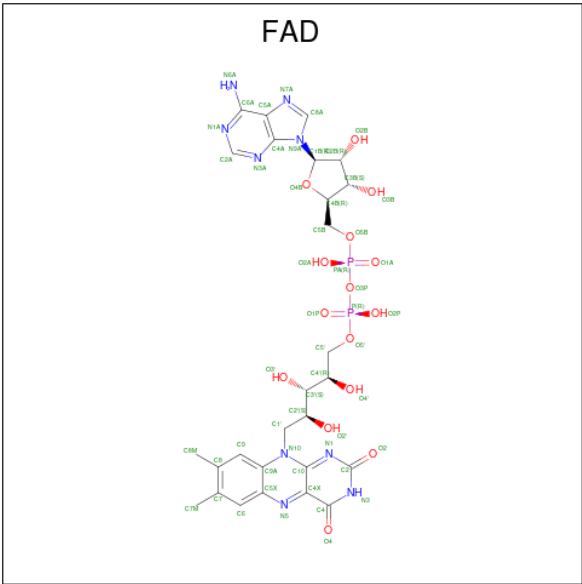
Chain	Residue	Modelled	Actual	Comment	Reference
A	-17	MET	-	initiating methionine	UNP Q8PYK9
A	-16	GLY	-	expression tag	UNP Q8PYK9
A	-15	SER	-	expression tag	UNP Q8PYK9
A	-14	SER	-	expression tag	UNP Q8PYK9
A	-13	HIS	-	expression tag	UNP Q8PYK9
A	-12	HIS	-	expression tag	UNP Q8PYK9
A	-11	HIS	-	expression tag	UNP Q8PYK9
A	-10	HIS	-	expression tag	UNP Q8PYK9
A	-9	HIS	-	expression tag	UNP Q8PYK9
A	-8	HIS	-	expression tag	UNP Q8PYK9
A	-7	SER	-	expression tag	UNP Q8PYK9
A	-6	SER	-	expression tag	UNP Q8PYK9
A	-5	GLY	-	expression tag	UNP Q8PYK9
A	-4	LEU	-	expression tag	UNP Q8PYK9
A	-3	VAL	-	expression tag	UNP Q8PYK9
A	-2	PRO	-	expression tag	UNP Q8PYK9
A	-1	ARG	-	expression tag	UNP Q8PYK9
A	0	GLY	-	expression tag	UNP Q8PYK9
A	1	SER	-	expression tag	UNP Q8PYK9
A	2	HIS	-	expression tag	UNP Q8PYK9
A	377	THR	MET	engineered mutation	UNP Q8PYK9

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



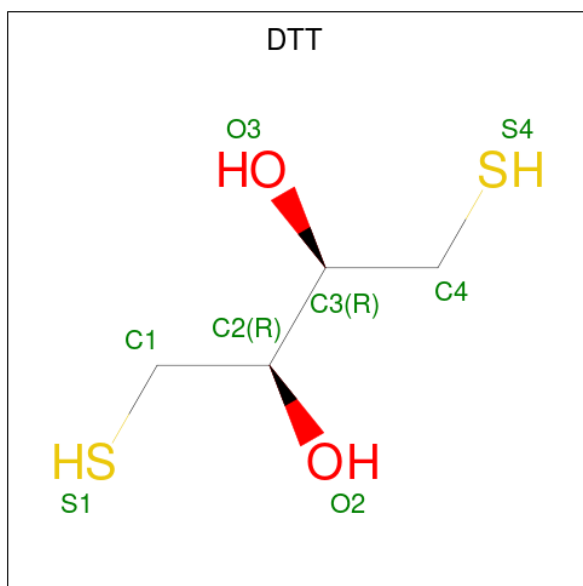
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is FLAVIN-ADENINE DINUCLEOTIDE (CCD ID: FAD) (formula: C₂₇H₃₃N₉O₁₅P₂) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

- Molecule 4 is 2,3-DIHYDROXY-1,4-DITHIOBUTANE (CCD ID: DTT) (formula: $C_4H_{10}O_2S_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	O	S	0	0
			8	4	2	2		

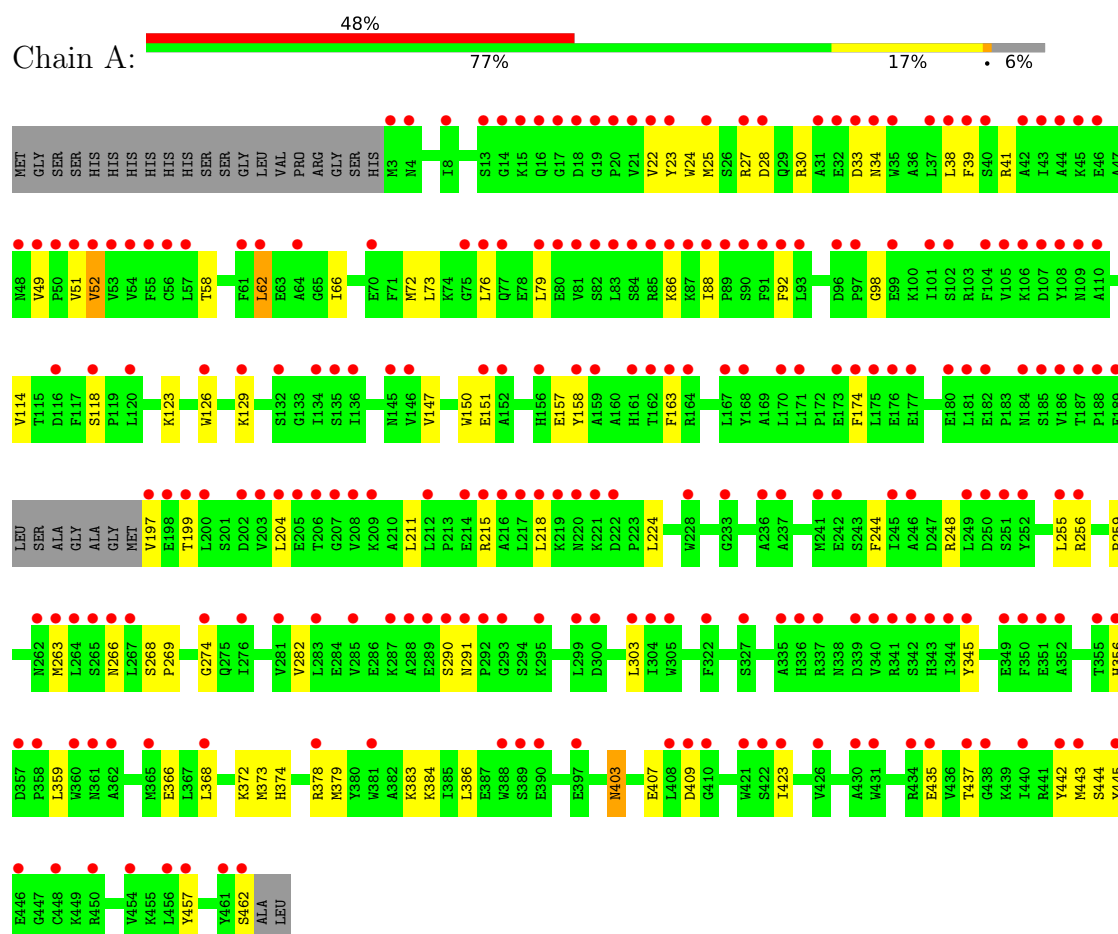
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	188	Total	O	0	0
			188	188		

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: DNA photolyase



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	70.52Å 70.52Å 246.18Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	31.68 – 2.50 31.68 – 2.50	Depositor EDS
% Data completeness (in resolution range)	100.0 (31.68-2.50) 99.9 (31.68-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.41 (at 2.00Å)	Xtriage
Refinement program	PHENIX (1.19_4092: ???)	Depositor
R, R_{free}	0.223 , 0.248 0.279 , 0.292	Depositor DCC
R_{free} test set	2095 reflections (1.85%)	wwPDB-VP
Wilson B-factor (Å ²)	15.3	Xtriage
Anisotropy	0.009	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 43.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.85	EDS
Total number of atoms	3836	wwPDB-VP
Average B, all atoms (Å ²)	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.63% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: FAD, DTT, SO4

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.15	0/3692	0.28	0/5017

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3572	0	3341	53	0
2	A	15	0	0	0	0
3	A	53	0	28	0	0
4	A	8	0	10	4	0
5	A	188	0	0	4	0
All	All	3836	0	3379	53	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

All (53) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:158:TYR:CD1	1:A:158:TYR:CZ	2.38	1.03
1:A:379:MET:CE	4:A:505:DTT:H2	1.90	1.00
1:A:379:MET:HE1	4:A:505:DTT:H2	1.44	1.00
1:A:39:PHE:CG	1:A:39:PHE:CE1	2.40	0.97
1:A:379:MET:HE3	4:A:505:DTT:H2	1.69	0.75
1:A:378:ARG:NH2	1:A:407:GLU:OE1	2.23	0.71
1:A:379:MET:HE1	4:A:505:DTT:C2	2.24	0.63
1:A:51:VAL:HG23	1:A:88:ILE:HG23	1.87	0.57
1:A:86:LYS:NZ	5:A:619:HOH:O	2.39	0.56
1:A:383:LYS:HD2	1:A:443:MET:HG3	1.86	0.56
1:A:378:ARG:NH2	1:A:407:GLU:CD	2.66	0.54
1:A:256:ARG:NH1	5:A:620:HOH:O	2.40	0.54
1:A:118:SER:HB3	1:A:123:LYS:HG2	1.89	0.54
1:A:266:ASN:HA	1:A:372:LYS:HE3	1.91	0.51
1:A:366:GLU:OE1	1:A:457:TYR:OH	2.22	0.51
1:A:66:ILE:HD12	1:A:215:ARG:HG3	1.93	0.50
1:A:92:PHE:O	1:A:197:VAL:N	2.45	0.49
1:A:150:TRP:CD1	1:A:151:GLU:HG2	2.48	0.49
1:A:386:LEU:HD13	1:A:423:ILE:HG23	1.95	0.48
1:A:224:LEU:HD13	1:A:368:LEU:HB3	1.96	0.48
1:A:373:MET:O	1:A:378:ARG:HD2	2.14	0.47
1:A:73[A]:LEU:HD23	1:A:204:LEU:HB2	1.96	0.47
1:A:129:LYS:HE3	1:A:129:LYS:HB2	1.63	0.47
1:A:403:ASN:ND2	1:A:403:ASN:C	2.73	0.47
1:A:41:ARG:HA	1:A:51:VAL:HG11	1.97	0.46
1:A:268:SER:OG	1:A:409:ASP:OD2	2.29	0.45
1:A:378:ARG:NH2	1:A:409:ASP:OD1	2.48	0.45
1:A:255:LEU:HB2	1:A:263:MET:HG2	1.99	0.44
1:A:98:GLY:HA3	1:A:129:LYS:HG2	1.98	0.44
1:A:27:ARG:NH2	5:A:615:HOH:O	2.48	0.44
1:A:345:TYR:OH	1:A:356:HIS:ND1	2.49	0.44
1:A:442:TYR:HE1	1:A:444:SER:HB3	1.82	0.44
1:A:123:LYS:NZ	5:A:605:HOH:O	2.35	0.43
1:A:62:LEU:HD12	1:A:211:LEU:HG	2.01	0.43
1:A:435:GLU:O	1:A:437:THR:N	2.46	0.43
1:A:28:ASP:HA	1:A:274:GLY:HA3	2.01	0.43
1:A:72:MET:O	1:A:76:LEU:HG	2.18	0.43
1:A:259:PRO:HA	1:A:374:HIS:CD2	2.53	0.43
1:A:23:TYR:CE2	1:A:25:MET:HB2	2.54	0.43
1:A:58:THR:HG21	1:A:126[B]:TRP:CZ2	2.53	0.43
1:A:157:GLU:HG3	1:A:163:PHE:CD1	2.54	0.42
1:A:22:VAL:HA	1:A:52:VAL:HG23	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:384:LYS:HD3	1:A:384:LYS:HA	1.81	0.42
1:A:24:TRP:N	1:A:114:VAL:O	2.40	0.42
1:A:244:PHE:HD1	1:A:248:ARG:HB2	1.84	0.41
1:A:34:ASN:O	1:A:38:LEU:HD12	2.20	0.41
1:A:62:LEU:HA	1:A:211:LEU:HD21	2.00	0.41
1:A:30:ARG:NE	1:A:33:ASP:O	2.44	0.41
1:A:147:VAL:HG13	1:A:174:PHE:CD2	2.55	0.41
1:A:282:VAL:HG21	1:A:303:LEU:HD21	2.02	0.41
1:A:290:SER:HB2	1:A:291:ASN:H	1.74	0.41
1:A:359:LEU:HB2	1:A:445:TYR:HE1	1.86	0.41
1:A:268:SER:OG	1:A:269:PRO:HD3	2.21	0.41

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	456/482 (95%)	439 (96%)	17 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	355/416 (85%)	347 (98%)	8 (2%)	44 72

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	49	VAL
1	A	52	VAL
1	A	62	LEU
1	A	79	LEU
1	A	199	THR
1	A	218	LEU
1	A	403	ASN
1	A	462	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

5 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	SO4	A	501	-	4,4,4	0.23	0	6,6,6	0.08	0
2	SO4	A	502	-	4,4,4	0.24	0	6,6,6	0.08	0
4	DTT	A	505	-	7,7,7	0.34	0	4,8,8	0.63	0
3	FAD	A	503	-	58,58,58	3.54	28 (48%)	85,89,89	2.11	24 (28%)
2	SO4	A	504	-	4,4,4	0.24	0	6,6,6	0.08	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	DTT	A	505	-	-	3/8/8/8	-
3	FAD	A	503	-	-	5/34/50/50	0/6/6/6

All (28) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	503	FAD	PA-O3P	7.99	1.68	1.59
3	A	503	FAD	O2'-C2'	-7.50	1.27	1.43
3	A	503	FAD	P-O3P	7.46	1.67	1.59
3	A	503	FAD	O4'-C4'	-6.93	1.28	1.43
3	A	503	FAD	C3B-C4B	-6.78	1.35	1.53
3	A	503	FAD	C4'-C3'	-6.58	1.41	1.53
3	A	503	FAD	C9A-N10	-6.47	1.29	1.41
3	A	503	FAD	O4-C4	5.94	1.34	1.23
3	A	503	FAD	C2'-C3'	-5.89	1.43	1.53
3	A	503	FAD	C2B-C1B	-5.76	1.35	1.53
3	A	503	FAD	C2B-C3B	-5.72	1.37	1.53
3	A	503	FAD	C8A-N9A	-5.69	1.27	1.37
3	A	503	FAD	O2-C2	5.46	1.35	1.24
3	A	503	FAD	C6A-N6A	4.53	1.45	1.34
3	A	503	FAD	C4-N3	-4.29	1.30	1.38
3	A	503	FAD	O3'-C3'	-3.56	1.34	1.43
3	A	503	FAD	C4A-N9A	-3.53	1.30	1.37
3	A	503	FAD	C1B-N9A	-3.47	1.36	1.46
3	A	503	FAD	P-O5'	2.94	1.70	1.59
3	A	503	FAD	C5B-C4B	-2.87	1.42	1.51
3	A	503	FAD	C2-N3	-2.69	1.33	1.39
3	A	503	FAD	C10-N10	-2.63	1.31	1.37
3	A	503	FAD	PA-O5B	2.54	1.69	1.59
3	A	503	FAD	PA-O2A	2.51	1.67	1.55

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	503	FAD	C8M-C8	2.46	1.55	1.51
3	A	503	FAD	P-O2P	2.32	1.66	1.55
3	A	503	FAD	C5X-N5	-2.24	1.35	1.39
3	A	503	FAD	C5A-C4A	2.15	1.42	1.39

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	503	FAD	C4A-N9A-C8A	8.41	114.56	105.74
3	A	503	FAD	C5A-C4A-N3A	-5.62	118.98	126.72
3	A	503	FAD	N3A-C4A-N9A	5.59	136.67	127.17
3	A	503	FAD	C4A-C5A-N7A	-4.56	105.37	110.58
3	A	503	FAD	N3A-C2A-N1A	-4.26	122.13	128.58
3	A	503	FAD	C5X-N5-C4X	-4.25	111.21	118.09
3	A	503	FAD	N9A-C8A-N7A	-3.93	108.37	113.94
3	A	503	FAD	C5'-C4'-C3'	-3.59	105.44	112.22
3	A	503	FAD	C2A-N3A-C4A	3.43	120.21	111.83
3	A	503	FAD	C4X-C10-N1	-3.41	116.23	124.59
3	A	503	FAD	C4X-C10-N10	3.10	120.91	116.48
3	A	503	FAD	C4-N3-C2	-2.98	120.36	125.64
3	A	503	FAD	C4X-C4-N3	2.94	120.73	113.25
3	A	503	FAD	C4B-O4B-C1B	-2.87	103.12	109.47
3	A	503	FAD	C9A-N10-C10	-2.69	116.65	120.75
3	A	503	FAD	C6A-C5A-N7A	2.50	136.91	132.09
3	A	503	FAD	C5A-N7A-C8A	2.48	107.35	103.45
3	A	503	FAD	C4-C4X-N5	-2.47	114.79	118.21
3	A	503	FAD	C5X-C9A-N10	2.39	120.13	117.97
3	A	503	FAD	O4-C4-C4X	-2.33	120.39	126.53
3	A	503	FAD	C4A-N9A-C1B	-2.13	121.66	126.63
3	A	503	FAD	C3B-C2B-C1B	2.12	105.47	101.46
3	A	503	FAD	C4-C4X-C10	2.11	120.55	116.93
3	A	503	FAD	C10-N1-C2	2.05	121.29	116.85

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	503	FAD	N10-C1'-C2'-C3'
4	A	505	DTT	C1-C2-C3-O3
4	A	505	DTT	O2-C2-C3-O3
4	A	505	DTT	O2-C2-C3-C4
3	A	503	FAD	P-O3P-PA-O1A

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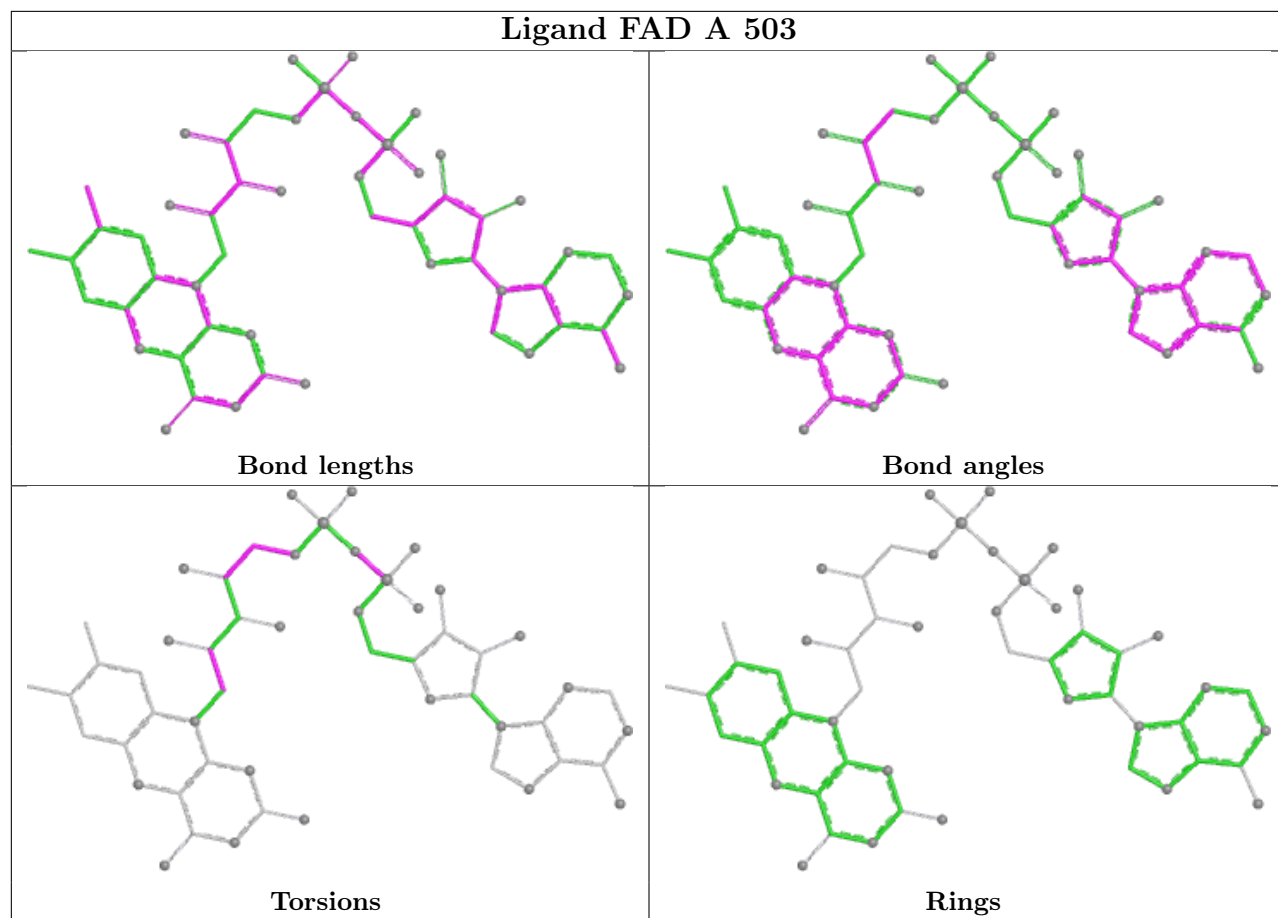
Mol	Chain	Res	Type	Atoms
3	A	503	FAD	O4'-C4'-C5'-O5'
3	A	503	FAD	C4'-C5'-O5'-P
3	A	503	FAD	P-O3P-PA-O2A

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	505	DTT	4	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	453/482 (93%)	2.17	229 (50%) 0 0	27, 53, 69, 90	10 (2%)

All (229) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	197	VAL	5.9
1	A	16	GLN	5.8
1	A	220	ASN	5.3
1	A	39	PHE	5.2
1	A	62	LEU	5.2
1	A	291	ASN	5.1
1	A	262	ASN	5.1
1	A	52	VAL	5.0
1	A	84	SER	5.0
1	A	219	LYS	4.9
1	A	362	ALA	4.9
1	A	174	PHE	4.9
1	A	337	ARG	4.9
1	A	233	GLY	4.7
1	A	202	ASP	4.6
1	A	186	VAL	4.6
1	A	198	GLU	4.6
1	A	250[A]	ASP	4.5
1	A	218	LEU	4.5
1	A	18	ASP	4.4
1	A	421	TRP	4.3
1	A	107	ASP	4.2
1	A	189	GLU	4.2
1	A	462	SER	4.2
1	A	49	VAL	4.2
1	A	132	SER	4.1
1	A	55	PHE	4.1

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Mol	Chain	Res	Type	RSRZ
1	A	82	SER	4.1
1	A	162	THR	4.1
1	A	53	VAL	4.1
1	A	342	SER	4.0
1	A	442	TYR	4.0
1	A	17	GLY	3.9
1	A	13	SER	3.9
1	A	38	LEU	3.9
1	A	221	LYS	3.8
1	A	40	SER	3.8
1	A	96	ASP	3.8
1	A	249	LEU	3.7
1	A	86	LYS	3.7
1	A	381	TRP	3.7
1	A	290	SER	3.7
1	A	343	HIS	3.7
1	A	263	MET	3.7
1	A	388	TRP	3.6
1	A	216	ALA	3.6
1	A	83	LEU	3.6
1	A	187	THR	3.6
1	A	48	ASN	3.6
1	A	45	LYS	3.6
1	A	158	TYR	3.6
1	A	246	ALA	3.6
1	A	350	PHE	3.6
1	A	182	GLU	3.5
1	A	46	GLU	3.5
1	A	22	VAL	3.5
1	A	168	TYR	3.5
1	A	431	TRP	3.5
1	A	443	MET	3.5
1	A	34	ASN	3.4
1	A	205	GLU	3.4
1	A	44	ALA	3.4
1	A	251	SER	3.4
1	A	85	ARG	3.4
1	A	199	THR	3.4
1	A	203	VAL	3.4
1	A	355	THR	3.4
1	A	176	GLU	3.4
1	A	108	TYR	3.3

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Mol	Chain	Res	Type	RSRZ
1	A	236	ALA	3.3
1	A	188	PRO	3.3
1	A	109	ASN	3.2
1	A	167	LEU	3.2
1	A	204	LEU	3.2
1	A	102	SER	3.2
1	A	54	VAL	3.2
1	A	215	ARG	3.2
1	A	134	ILE	3.2
1	A	51	VAL	3.1
1	A	146	VAL	3.1
1	A	42	ALA	3.1
1	A	90	SER	3.1
1	A	267	LEU	3.1
1	A	161	HIS	3.1
1	A	445	TYR	3.0
1	A	289	GLU	3.0
1	A	292	PRO	3.0
1	A	33	ASP	3.0
1	A	3	MET	3.0
1	A	145	ASN	3.0
1	A	99	GLU	3.0
1	A	222	ASP	3.0
1	A	357	ASP	3.0
1	A	81	VAL	2.9
1	A	344	ILE	2.9
1	A	152	ALA	2.9
1	A	228	TRP	2.9
1	A	336	HIS	2.9
1	A	356	HIS	2.9
1	A	25	MET	2.9
1	A	32	GLU	2.9
1	A	181	LEU	2.9
1	A	23	TYR	2.9
1	A	434	ARG	2.9
1	A	264	LEU	2.9
1	A	241	MET	2.9
1	A	20	PRO	2.9
1	A	92	PHE	2.9
1	A	151	GLU	2.8
1	A	390	GLU	2.8
1	A	208	VAL	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	437	THR	2.8
1	A	116	ASP	2.8
1	A	214	GLU	2.8
1	A	91	PHE	2.8
1	A	43	ILE	2.8
1	A	245	ILE	2.8
1	A	266	ASN	2.8
1	A	21	VAL	2.8
1	A	448	CYS	2.8
1	A	104	PHE	2.8
1	A	77	GLN	2.7
1	A	101	ILE	2.7
1	A	57	LEU	2.7
1	A	322	PHE	2.7
1	A	454	VAL	2.7
1	A	212	LEU	2.7
1	A	255	LEU	2.7
1	A	360	TRP	2.7
1	A	256	ARG	2.7
1	A	79	LEU	2.7
1	A	80	GLU	2.7
1	A	89	PRO	2.6
1	A	106	LYS	2.6
1	A	163	PHE	2.6
1	A	173	GLU	2.6
1	A	252	TYR	2.6
1	A	345	TYR	2.6
1	A	435	GLU	2.6
1	A	287	LYS	2.6
1	A	35	TRP	2.6
1	A	440	ILE	2.6
1	A	105	VAL	2.6
1	A	206	THR	2.6
1	A	274	GLY	2.5
1	A	352	ALA	2.5
1	A	339	ASP	2.5
1	A	61	PHE	2.5
1	A	217	LEU	2.5
1	A	87	LYS	2.5
1	A	156	HIS	2.5
1	A	184	ASN	2.5
1	A	237	ALA	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	327	SER	2.5
1	A	97	PRO	2.5
1	A	283	LEU	2.5
1	A	361	ASN	2.5
1	A	378	ARG	2.5
1	A	50	PRO	2.5
1	A	200	LEU	2.5
1	A	281	VAL	2.5
1	A	129	LYS	2.4
1	A	461	TYR	2.4
1	A	88	ILE	2.4
1	A	136	ILE	2.4
1	A	276	ILE	2.4
1	A	457	TYR	2.4
1	A	365[A]	MET	2.4
1	A	335	ALA	2.4
1	A	31	ALA	2.4
1	A	295	LYS	2.4
1	A	446	GLU	2.4
1	A	70	GLU	2.3
1	A	349	GLU	2.3
1	A	397	GLU	2.3
1	A	126[A]	TRP	2.3
1	A	171	LEU	2.3
1	A	285	VAL	2.3
1	A	177	GLU	2.3
1	A	299	LEU	2.3
1	A	28	ASP	2.3
1	A	340	VAL	2.3
1	A	410	GLY	2.3
1	A	170	LEU	2.3
1	A	303	LEU	2.3
1	A	304	ILE	2.3
1	A	110	ALA	2.2
1	A	37	LEU	2.2
1	A	93	LEU	2.2
1	A	242	GLU	2.2
1	A	27	ARG	2.2
1	A	422	SER	2.2
1	A	456	LEU	2.2
1	A	164	ARG	2.2
1	A	341	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	15	LYS	2.2
1	A	426	VAL	2.1
1	A	159	ALA	2.1
1	A	430	ALA	2.1
1	A	76	LEU	2.1
1	A	368	LEU	2.1
1	A	408	LEU	2.1
1	A	8	ILE	2.1
1	A	265	SER	2.1
1	A	300[A]	ASP	2.1
1	A	409	ASP	2.1
1	A	64	ALA	2.1
1	A	14	GLY	2.1
1	A	423	ILE	2.1
1	A	358	PRO	2.1
1	A	4	ASN	2.1
1	A	209	LYS	2.1
1	A	185	SER	2.1
1	A	56[A]	CYS	2.1
1	A	450	ARG	2.0
1	A	19	GLY	2.0
1	A	75	GLY	2.0
1	A	180	GLU	2.0
1	A	207	GLY	2.0
1	A	438	GLY	2.0
1	A	389	SER	2.0
1	A	120	LEU	2.0
1	A	175	LEU	2.0
1	A	288	ALA	2.0
1	A	351	GLU	2.0
1	A	293	GLY	2.0
1	A	305	TRP	2.0
1	A	118	SER	2.0
1	A	135	SER	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

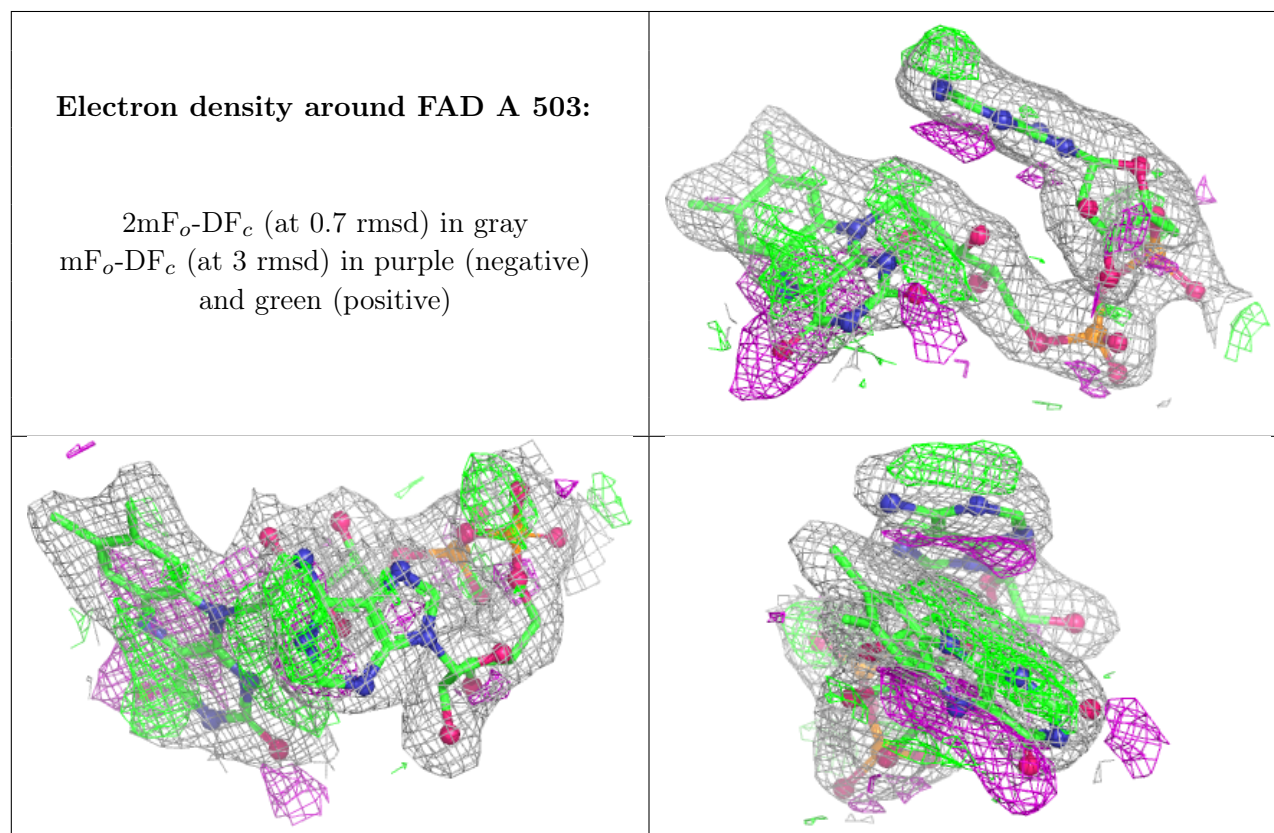
There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	SO4	A	504	5/5	0.57	0.18	96,100,103,104	5
4	DTT	A	505	8/8	0.69	0.35	35,38,43,44	8
2	SO4	A	502	5/5	0.75	0.25	64,65,66,69	0
3	FAD	A	503	53/53	0.83	0.20	35,36,42,54	0
2	SO4	A	501	5/5	0.94	0.13	37,44,51,52	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



6.5 Other polymers ⓘ

There are no such residues in this entry.